AMENDMENTS TO THE SPECIFICATION:

Please amend the specification as follows:

Please delete the paragraph on page 5, lines 15-17 and replace it with the following paragraph:

Fig. 1 comprises partial DNA (SEQ ID NO: 1) and derived amino acid sequence (SEQ ID NO: 2) of bovine BMP-2 from bacteriophage lambda bP-21, ATCC #40310 further described below.

Please delete the paragraph on page 5, lines 19-21 and replace it with the following paragraph:

Fig. 2 sets forth the DNA (SEQ ID NO: 3) and derived amino acid sequence (SEQ ID NO: 4) of human BMP-2 from lambda U2OS-39, ATCC #40345 further described below.

Please delete the paragraph on page 5, lines 23-25 and replace it with the following paragraph:

Fig. 3 sets forth the DNA (SEQ ID NO: 5) and derived amino acid sequence (SEQ ID NO: 6) of human BMP-4 from lambda U2OS-3, ATCC #40342 further described below.

Please delete the paragraph on page 19, lines 16-28 and replace it with the following paragraph:

The protein composition of Example IIA of molecular weight 28 – 30 kd is reduced as described in Example IIC and digested with trypsin. Eight tryptic fragments are isolated by standard procedures having the following amino acid sequences:

Fragment 1: A A F L G D I A L D E E D L G (SEQ ID NO: 7)

Fragment 2: A F Q V Q Q A A D L (SEQ ID NO: 8)

Fragment 3: N Y Q D M V V E G (SEQ ID NO: 9)

Fragment 4: S T P A Q D V S R (SEQ ID NO: 10)

Fragment 5: N Q E A L R (SEQ ID NO: 11)

Fragment 6: L S E P D P S H T L E E (SEQ ID NO: 12)

Fragment 7: F D A Y Y (SEQ ID NO: 13)

Fragment 8: L K P S N ? A T I Q S I V E (SEQ ID NO: 14)

Please delete the paragraph on page 19, line 30 to page 20, line 1 and replace it with the following paragraph, recognizing that J. Mol. Biol. Was underlined in the original:

Two probes consisting of pools of oligonucleotides (or unique oligonucleotides) are designed according to the method of R. Lathe, J. Mol. Biol., 183(1) : 1-12 (1985) on the basis of the amino acid sequence of Fragment 3 and synthesized on an automated DNA synthesizer as described above.

Probe #1: A C N A C C A T [A/G] T C [T/C] T G [A/G] A T (SEQ ID NO: 15)

Probe # 2: C A [A/G] G A [T/C] A T G G T N G T N G A (SEQ ID NO: 16)

Please delete the paragraph on page 24, line 34 to page 26, line 8 and replace it with the following paragraph:

Full-length BMP-4 human cDNA clones are obtained in the following manner. The 200 bp EcoRI-SacI fragment from the 5' end of the BMP-4 recombinant II-10-1 is

isolated from its plasmid subclone, labeled by nick-translation, and hybridized to a set of duplicate nitrocellulose replicas of the U-2 OS cDNA library (25 filters/set; representing 500,000 recombinants). Hybridization and washing are performed under stringent conditions as described above. 16 duplicate positives are picked and replated for secondaries. Nitrocellulose filter replicas of the secondary plates are made and hybridized to an oligonucleotide which was synthesized to correspond to the sequence of Il-10-1 and is of the following sequence:

CGGGCGCTCAGGATACTCAAGACCAGTGCTG (SEQ ID NO: 17)

Hybridization is in standard hybridization buffer AT 50° C with washing at 50° in 1 X SCC, 0.1% SDS. 14 recombinant bacteriophage which hybridize to this oligonucleotide are plague purified. Plate stocks are made and small scale bacteriophage DNA preparations made. After sucloning 3 of these into M13, sequence analysis indicates that they represent clones which overlap the original BMP-4 clone. One of these, lambda U2OS-3, was deposited with the ATCC under accession number 40342 in June 16, 1987. U2OS-3 contains an insert of approximately 1.8 kb. The DNA sequence (SEQ ID NO:5) and derived amino acid sequence (SEQ ID NO: 6) of U2OS-3 are shown below in Figure 3. This clone is expected to contain all of the nucleotide sequence necessary to encode the entire human BMP-4 protein. The BMP-4 protein encoded by Figure 3 is contemplated to contain the 97 amino acid sequence from amino acid #311 to #408 or a sequence substantially homologous thereto. This cDNA contains an open reading frame of 1224 bp, encoding a protein of 408 amino acids, preceded by a 5' untranslated region of 394 bp with stop codons in all frames, and contains a 3' untranslated region of 308 bp following the in-frame stop codon. The 8 bp

region preceding the 5' untranslated region represents a linker used in the cDNA cloning procedure. This protein of 408 amino acids has molecular weight of 47kd and is contemplated to represent the primary translation product. Mature BMP-4 is contemplated to comprise amino acid #293 (Ser, Pro, Lys...) - #408 (Arg) of Figure 3. A sequence similar though not identical to tryptic Fragment 3 of Example IV is underlined in Figure 3 (SEQ ID NO: 6). The underlined sequence Asn-Tyr-Gln-Glu-Met-Val-Val-Glu-Gly (residues 396-404 of SEQ ID NO: 6) differs from the tryptic fragment Asn-Tyr-Gln-Asp-Met-Val-Val-Glu-Gly (SEQ ID NO: 9) by one amino acid in position four.

Please delete the paragraph on page 30, lines 13-30 and replace it with the following paragraph with both E. coli and Biotechnology 84 underlined in the original:

Plasmid pMT2 CXM is obtained by EcoRI digestion of pMT2-VWF, which has been deposited with the American Type Culture Collection (ATCC) , Rockville, MD (USA) under accession number ATCC 67122. EcoRI digestion excises the cDNA insert present in pMT2-VWF, yielding pMT2 in linear form which can be ligated and used to transform E. coli HB 101or DH-5 to ampicillin resistance. Plasmid pMT2 DNA can be prepared by conventional methods. pMT2 CXM is then constructed using loopout/in mutagenesis [Morinaga, et al., Biotechnology 84: 636 (1987)]. This removes bases 1075 to 1145 relative to the Hind III site near the SV40 origin of replication and enhancer sequences of pMT2. In addition it inserts the following sequence:

5' PO-$_c$ATGGGCAGCTCGAG-3' (SEQ ID NO: 18)

at nucleotide 1145. This sequence contains the recognition site for the restriction endonuclease Xho I. A derivative of pMT2CXM, termed pMT23, contains recognition

sites for the restriction endonucleases PstI, Eco RI, SalI and XhoI. Plasmid pMT2 CXM and pMT23 DNA may be prepared by conventional methods.

Please delete the paragraph on page 31, lines 13-27 and replace it with the following paragraph with the nucleotide sequences underlined in the original:

A derivative of the BMP-2 cDNA sequence set fourth in Figure 2 (SEQ ID NO: 3) in which the 5' untranslated region is deleted ~~is made~~ by removal of the sequences contained between the SalI site at the 5' adapter (from the original cDNA cloning), and the SalI site 7 base pairs upstream of the initiator ATG, by digestion with SalI and religation. This step is conveniently performed in either SP65 derivatives containing the full length BMP-2 cDNA, but can also be performed in pMT2 derivatives. The 3' untranslated region is removed using heteroduplex mutagenesis using the mutagenic oligonucleotide

5' GAGGGTTGTGGGTGTCGCTAGTGAGTCGACTACAGCAAAATT (SEQ ID NO: 19)
Terminator SalI

The sequence contains the terminal 3' coding region of the BMP-2 cDNA, followed immediately by a recognition site for SalI.

Please delete the paragraph on page 33, line 25 to page 34, line 4 and replace it with the following paragraph with the nucleotide sequences underlined in the original:

pMT21 was derived from pMT2 through the following two modifications. First, 76 bp of the 5' untranslated region of the DHFR cDNA including a stretch of 19 G residues

from G/C tailing for cDNA cloning was deleted. In this process, a XhoI site was inserted to obtain the following sequence immediately upstream from DHFR:

5' -CTGCAGGCGAGCCTGAATTCCTCGAGCCATCATG-3' (SEQ ID NO: 20)
PstI Eco RI XhoI

Second, a unique ClaI site was introduced by digestion with EcoRV and XbaI, treatment with Klenow fragment of DNA polymerase I, and ligation to a ClaI linker (CATCGATG). This deletes a 250 bp segment from the adenovirus virus associated RNA (VAI) region but does not interfere with VAI RNA gene expression or function. pMT21 was digested with EcoRI and XhoI, and used to derive the vector pEMC2B1.

Please delete the paragraph on page 34, lines 5-26 and replace it with the following paragraph with J. Virol. 63 and the nucleotide sequences underlined in the original:

A portion of the EMCV leader was obtained fromm pMT2-ECAT1 [S.K. Jung, et al, J. Virol 63: 1651-1660 (1989)] by digest with Eco RI and PstI, resulting in a 2752 bp fragment. This fragment was digested with TaqI yielding an Eco RI-TaqI fragment of 508 bp which was purified by electrophoresis on low melting agarose gel. A 68 bp adapter and its complementart strand were synthesized with a 5' TaqI protruding end and a 3' XhoI protruding end which has the following sequence:

5'-CGAGGTTAAAAAACGTCTAGGCCCCCCGAACCACGGGGACGTGGTTTTCCTTT
TaqI

GAAAAACACGATTGC-3' (SEQ ID NO: 21)
XhoI

This sequence matches the EMC virus leader sequence from nucleotide 763 to 827. It also changes the ATG at position 10 within the EMC virus leader to an ATT and is followed by a XhoI site. A three way ligation of the pMT21 Eco RI-XhoI fragment, the EMC virus EcoRI-TaqI fragment, and the 68 bp oligonucleotide adapter TaqI-XhoI adapter resulted in the vector pEMC2B1.

Please delete the paragraph on page 34, line 35 to page 35 and replace it with the following paragraph with the nucleotide sequences underlined in the original:

A derivative of the BMP-4 cDNA sequence set forth in Figure 3 in which the 3' untraslated region is removed ~~is made~~ via heteroduplex mutagenesis with the mutagentic oligonucleotide:

5' GGATGTGGGTGCCGCTGACTCTAGAGTCGACGGAATTC 3' (SEQ ID NO: 22).
Terminator EcoRI

This deletes all of the sequences 3' to the translation terminator codon of the BMP-4 cDNA, juxtaposing this terminator codon and the vector polylinker sequences. This step is performed in an SP65 vector though may be conviently performed in MT2 derivatives containing the BMP-4 cDNA. The 5' untraslated region is removed using the restriction endonuclease BsmI, which cleaves within the eighth codon of BMP-4 cDNA. Reconstruction of the first eighth codon of BMP-4 cDNA. Reconstruction of the first eight codons is accomplished by ligation to oliognucleotides:

EcoRI Initiator BsmI
5' AATTCACCATGATTCCTGGTAACCGAATGCT 3' and
3' GTGGTACTAAGGACCATTGGCTTAC 5' (SEQ ID NO: 23)

These oligonucleotides form a duplex which has a BsmI complementary cohesive end capable of ligation to the BsmI restricted BMP-4 cDNA, and it has an EcoRI complementary cohesive end capable of ligation to the EcoRI restricted vector MT2. Thus the cDNA for BMP-4 with the 5' and 3' untranslated regions deleted, and retaining the entire encoding sequence is contained within an EcoRI restriction fragment of approximately 1.2kb.